RAD51 and XRCC3 gene polymorphisms and the risk of developing acute myeloid leukemia

Hamdy MS, El-Haddad AM, Bahaa El-Din NM, Makhlouf MM, Abdel-Hamid SM.

Department of Clinical and Chemical Pathology, Faculty of Medicine, El-Kasr El-Aini Hospital, Cairo, Egypt.

Abstract

RAD51 (Rec A homolog of E. coli) is a polymorphic gene and one of the central proteins in homologous recombination-DNA-double-stand breaks (HR-DNA-DSB) repair pathway, which is vital in maintaining genetic stability within a cell. The x-ray repair cross complementing (XRCC3) protein also functions in HR-DNA-DSB repair pathway and directly interacts with and stabilizes RAD51 and the closely related RAD51C. The aim of this study was to determine the prevalence of the RAD51 and XRCC3 repair gene polymorphisms among acute myeloid leukemia (AML) patients and to define their role in development of AML and its correlation with the clinical presentation, laboratory data as well as treatment outcome using polymerase chain reaction-restriction fragment length polymorphism assay in 50 de novo AML patients as well as 30 healthy subjects as a control group. Our study revealed that RAD51 G135C and XRCC3 Thr241Met alleles were associated with increased risk of AML with odds ratio (OR) of 2.833 and 2.909 and 95% confidence interval (CI) of 1.527 to 8.983 and 1.761 to 9.788, respectively. Moreover, when combining the 2 genes polymorphisms, a significant elevation of the risk of AML was found with OR of 3.124 and 95% CI of 1.872 to 11.243. As regards treatment outcome, a highly statistical significant difference was found between XRCC3 genotypes with P value of 0.001, whereas no significant difference was present between RAD51 genotypes with P value of 0.29. This clarifies that XRCC3 gene polymorphisms was found to have a significant impact on the risk of treatment failure with OR of 3.560 and 95% CI of 1.167 to 10.875; however, RAD51 gene polymorphism was not found to have an equivalent effect with OR of 2.813 and 95% CI of 0.933 to 10.828. So XRCC3 gene polymorphism might be considered as a prognostic marker in AML. In conclusion, RAD51 and XRCC3 genes polymorphisms may play an important role in the development of AML.